



SEQUENCE LISTING

<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> Walker\_2500\_097US2

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

C  
<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)..(624)

<223> This is the codon for the substituted amino acids  
of the mutated sequence.

<400> 1

aacatgaaca tcaaaggatc gccatggaaa gggccctcc tgctgctgct ggtgtcaaac 60  
ctgctgctgt gccagacgt ggcccccttg cccatctgtc cggcggggc tgcccgatgc 120  
caggtagcc ttccgacacct gtttgaccgc gccgtcgcc tggccacta catccataac 180  
ctctcctcag aaatgttcag cgaattcgat aaacgggtata cccatggccg ggggttcatt 240  
accaaggcca tcaacagctg ccacacttct tcccttgcca ccccccgaaga caaggagcaa 300  
gccaacacaga tgaatcaaaa agactttctg agcctgtatag tcagcatatt gcgatcctgg 360  
aatgagcctc tggatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420  
atccatatcca aagctgtaga gattgaggag caaacaaac ggcttctaga gggcatggag 480  
ctgatagtca gccaggttca tcctgaaacc aaagaaaaatg agatctaecc tgcgtggc 540  
ggacttccat ccctgcagat ggctgtatgaa ggtctcgcc tttctgctta ttataaccctg 600  
ctccactgcc tacgcaggaa tnnncataaaa atcgacaatt atctcaagct cctgaagtgc 660  
cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcattatctt ctgagaaggt 720  
ccttaatgtat ccgttccatt gcaagcttct ttttagttgtatcttttga atccatgctt 780  
gggtgtaaaca ggtctccctt taaaaataa aaactgactc gtttagagaca tc 832

<210> 2  
<211> 228  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (208)  
<223> Site mutated codon where the normal codon coding  
for serine is modified preferably to encode for  
aspartate or glutamate, most preferably aspartate.

<400> 2  
Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu  
1 5 10 15  
Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile  
20 25 30  
Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe  
35 40 45  
Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu  
50 55 60  
Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile  
65 70 75 80  
Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu  
85 90 95  
Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu  
100 105 110  
Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val  
115 120 125  
Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys  
130 135 140  
Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu  
145 150 155 160  
Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr  
165 170 175  
Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser  
180 185 190

Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa  
195 200 205  
His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His  
210 215 220  
Asn Asn Asn Cys  
225

<210> 3  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: This sequence  
is a primer.

<400> 3  
gcagggatga ccacaagg tt gac

23

<210> 4  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: This sequence  
is a primer.

<220>  
<221> variation  
<222> (12)  
<223> This is a codon that can be replaced for nucleic  
acid substitutes.

<400> 4  
cgcaaggat gnacacaagg ttga

24

<210> 5  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: This sequence  
is a primer.

<220>  
<221> variation  
<222> (12)  
<223> This is a codon that can be replaced for nucleic  
acid substitutes.

<400> 5  
acgcaggat gnkataaaat cg

22

<210> 6  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: This sequence  
is a primer.

<400> 6  
cgtggccccc atatgttgcc catctg

26